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a plurality of different peptides, all peptides of said panel being the same length, each library having at least two constant residue positions, one at a first position and the other at a second position,

where the first position is fixed for all libraries in the panel, and is assigned the same residue for all peptides in any given library, but libraries of the panel collectively present a plurality of different residues at said first position,

where said first position is (a) at least five amino acids from both ends of the peptides, or (b) is in the middle 50% of the peptides,

where said panel comprises a plurality of subpanels, each comprising a plurality of libraries, and in each subpanel, the location of the second position is constant, but said location varies from subpanel to subpanel so the second positions of said subpanels, collectively scan a plurality of residue positions other than said first position,

where the second position is assigned the same residue for all peptides in a given library but the libraries of a given subpanel collectively present a plurality of different residues at said second position,

where if said libraries comprise more than two constant residue positions, the constant residue positions other than said first and second positions are constant for all peptides in said panel,

where one or more of the other positions of said libraries are variable positions, at which a given library exhibits a plurality of different residues as a result of sequence variation from peptide to peptide,

each library being a separate and physically distinct entity from the other libraries of the panel.

33 (twice amended). A structured panel of biased combinatorial linear peptide libraries, each library comprising

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a plurality of different peptides, all peptides of said panel being the same length, each library having at least two biased residue positions, one at a first position and another at a second position, the amino acids allowed in each library at said biased positions being only a subset of the set of amino acids allowed at the remaining positions of said library, and also being only a subset of the set of amino acids allowed at that biased position in the panel as a whole,

where the first position is fixed for all libraries in the panel,

where said first position is (a) at least five amino acids from both ends of the peptides, or (b) is in the middle 50% of the peptides,

where said panel comprises a plurality of subpanels, each comprising a plurality of libraries, and in each subpanel, the location of the second position is constant, but said location varies from subpanel to subpanel so the second positions of said subpanels collectively scan a plurality of residue positions other than said first position,

where if said libraries comprise more than two constant residue positions, the constant residue positions other than said first and second positions are constant for all peptides in said panel,

each library being a separate and physically distinct entity from the other libraries of the panel.

35 (twice amended). A structured panel of biased combinatorial linear peptide libraries, each library comprising a plurality of different peptides, all peptides of said panel being the same length, each library having at least two biased residue positions, one at a first position and another at a second position, the amino acids allowed in each library at said biased positions being only a subset of the set amino acids allowed at the remaining positions of said library, and also

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being only a subset of the set of amino acids allowed at that biased position in the panel as a whole,

where the first position is fixed for all libraries in the panel,

where said first position is (a) at least five amino acids from both ends of the peptides, or (b) is in the middle 50% of the peptides,

where each library is obtained by mixing a plurality of different mixed oligonucleotides, each oligonucleotide comprising one fully variable codon and one less variable codon, the position of the less variable codon varying so that said plurality collectively scan also positions other than said first fixed position, said less variable codon encoding the second position of each peptide,

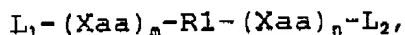
where if said libraries comprise more than two constant residue positions, the constant residue positions other than said first and second positions are constant for all peptides in said panel,

each library being a separate and physically distinct entity from the other libraries of the panel.

Please add the following new claims:

39 (new). The panel of claim 27, wherein there is no position which is the same amino acid for all peptides of the panel.

40 (new). The panel of claim 27 wherein said peptides are of the form



where L_1 and L_2 are each independently chosen from the group consisting of nothing and a subsequence of one or more amino acids, said subsequence being the same for all peptides of the panel,

$R1$ is the amino acid at said first position, and

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m and n are independently chosen from the range of 2 to 20.

41 (new). The panel of claim 27 wherein if L_1 or L_2 is a subsequence of one or more amino acids, the subsequence is not more than three amino acids.

42 (new). The panel of claim 41 in which L_1 is nothing, SS-, or SR-, and L_2 is nothing or -SR.

43 (new). The panel of claim 32 in which the second positions collectively scan all residue positions which are variable across the panel as a whole except for said first position.

44 (new). The panel of claim 33 in which the second positions collectively scan all residue positions which are variable across the panel as a whole except for said first position.

45 (new). The panel of claim 35 in which the second positions collectively scan all residue positions which are variable across the panel as a whole except for said first position.

46 (new). A structured panel consisting of a plurality of biased combinatorial linear peptide libraries, each library comprising a plurality of different peptides, all peptides of said panel being of the same length, there being in said peptides, either one position which is or two positions which are (1) for each library, the same amino acid (a "constant" amino acid) in that position in all peptides of that library, and (2) not the same amino acid in that position in all libraries of said panel,

at least one of said positions being fixed for all peptides in all libraries of said panel, said fixed position being (a) at least five residues from both ends of the peptides or (b) within the middle 50% of the peptides,

each library being a separate and physically distinct entity from all other libraries of the panel,